Amended Claims
37 CFR 1.121(c)(3)

21. (New) Method for the production of a nucleic acid molecule comprising the steps

a) providing an oligonucleotide which is prepared by the following steps:

aa) coupling one end of an oligonucleotide to a solid matrix wherein the coupling is effected by means of a modification and the oligonucleotide contains a recognition sequence for a type IIS restriction enzyme which cleaves outside its recognition sequence,

ab) adding an additional oligonucleotide which is at least partially double-stranded and contains a different recognition sequence than in step aa) for a type IIS restriction enzyme which cleaves outside its recognition sequence, whereby this oligonucleotide cannot bind to the matrix,

ac) ligating the oligonucleotides from steps aa) and ab) in the orientation determined by the blockage of the ends that are not to be ligated,

ad) removing non-consumed reactants and enzymes,

ae) cleaving the ligation product from step ac) with a type IIS restriction enzyme which cleaves outside its recognition sequence whereby the cleavage occurs in the nucleic acid sequence of the oligonucleotide from step ab),

af) separating the reaction mixture from the elongated oligonucleotide from step aa) obtained in step ae),

ag) repeating steps ab) to af) at least once,

b) Providing an additional oligonucleotide which is prepared by the following steps:

ba) coupling one end of an oligonucleotide to a solid matrix wherein the coupling is effected by means of a modification and the oligonucleotide contains a recognition sequence for a type IIS restriction enzyme which cleaves outside its recognition sequence,

bb) adding an additional oligonucleotide which is at least partially double-stranded and contains a different recognition sequence than in step ba) for a type IIS restriction enzyme which cleaves outside its recognition sequence, whereby this oligonucleotide cannot bind to the matrix,

bc) ligating the oligonucleotides from steps ba) and bb) in the orientation determined by the blockage of the ends that are not to be ligated,

bd) removing non-consumed reactants and enzymes,

be) cleaving the ligation product from step bc) with a type IIS restriction enzyme which cleaves outside its recognition sequence whereby the cleavage occurs in the oligonucleotide from step bb),

bf) separating the nucleic acid molecule elongated in this manner from the reaction mixture,

bg) repeating steps bb) to bf) at least once, wherein after the last ligation in step bc) and removing non-consumed reactants and enzymes, the ligation product is cleaved with a type IIS restriction enzyme whereby the cleavage occurs in the oligonucleotide from step ba),

c) ligating the oligonucleotides from steps a) and b) in the orientation determined by the blockage of the ends that are not to be ligated,

d) removing non-consumed reactants and enzymes,

e) cleaving the ligation product from step c) with a type IIS restriction enzyme which cleaves outside its recognition sequence whereby the cleavage occurs in the oligonucleotide from step a) or b),

f) separating the nucleic acid molecule elongated in this manner from the reaction mixture.

22. (New) Method as claimed in claim 21, wherein the oligonucleotide used in step ab) or bb) is a nucleic acid molecule produced by the method as claimed in claim 21.

23. (New) Method as claimed in claims 21 or 22, wherein an exonuclease and/or phosphatase reaction is carried out as step ac)', bc)' or c)' after step ac), bc) or c).

24. (New) Method as claimed in claim 23, wherein the reaction mixture of step ac'), bc)' or c)' is removed after the reaction.

25. (New) Method as claimed in one of the claims 21 to 23, wherein the end of the oligonucleotide from step a), aa) or ba) that is not coupled to the matrix contains a part of a recognition sequence for a type IIS restriction enzyme which cleaves outside its recognition sequence and the other part of the recognition sequence for this restriction enzyme is derived from the oligonucleotide from step ab), bb) or b).

26. (New) Method as claimed in claims 21 to 25, wherein the modification is a biotin residue, a digoxigenin residue, a fluorescein isothiocyanate residue, an amino compound or a succinyl ester.

27. (New) Method as claimed in one of the claims 21 to 26, wherein the oligonucleotide from step aa), ba) or a) and/or ab), bb) or b) has a loop.

28. (New) Method as claimed in claim 27, wherein the oligonucleotide from step aa), ba) or a) is coupled via a modification in the loop region to the solid matrix.

29. (New) Method as claimed in one of the claims 21 to 28, wherein the solid matrix is a bead, preferably made of glass or polystyrene, a microscope slide, a DNA chip, the well of a microtitre plate or a test tube.

30. (New) Method as claimed in one of the claims 21 to 29, wherein the solid matrix comprises a streptavidin residue, an anti-digoxigenin antibody or an anti-fluorescein isothiocyanate antibody.

31. (New) Method as claimed in one of the claims 21 to 30, wherein the oligonucleotides from steps aa), ba) or a) and ab), bb) or b) have mutually complementary single-strand overhangs at their ends to be ligated.

32. (New) Method as claimed in claim 31, wherein the single strand overhangs are 1, 2, 3, 4 or 5 nucleotides long.

33. (New) Method as claimed in claims 21 to 32, wherein the various type IIS restriction endonucleases are replaced by ribozymes which cleave in an analogous manner.

34. (New) Method as claimed in one of the claims 21 to 33, wherein the oligonucleotide in step ab), bb) or b) is a PCR product, a plasmid vector, a phage or viral DNA, an artificial chromosome or another synthetic DNA.

35. (New) Kit for the production of a nucleic acid sequence by the method as claimed in one of the claims 21 to 34, comprising:

a) a library of 1 to 1,048,576 different oligonucleotides wherein the oligonucleotides can be coupled to a solid matrix by means of a modification at one end and the oligonucleotide contains a recognition sequence or a part of the recognition sequence for a type IIS restriction enzyme which cleaves outside its recognition sequence,

b) an additional library of 4 to 1,048,576 different oligonucleotides wherein each of the oligonucleotides contains a recognition sequence for a type IIS restriction enzyme which cleaves outside its recognition sequence which is different from the type IIS restriction enzyme from aa), ba) or a) and optionally contains the other part of the recognition sequence of the restriction enzyme from step aa), ba) or a)

c) a solid matrix,

d) reservoirs for the enzymes required to produce the nucleic acid molecule and/or other reagents.

36. (New) Device for the automated production of a nucleic acid molecule by a method as claimed in one of the claims 21 to 34, characterized in that it contains

a) a library of 1 to 1,048,576 different oligonucleotides wherein the oligonucleotides can be coupled to a solid matrix by means of a modification at one end and the oligonucleotide contains a recognition sequence or a part of the recognition sequence for a type IIS restriction enzyme which cleaves outside its recognition sequence,

b) an additional library of 4 to 1,048,576 different oligonucleotides wherein each of the oligonucleotides contains a recognition sequence for a type IIS restriction enzyme which cleaves outside its recognition sequence which is different from the type IIS restriction enzyme from aa), ba) or a), and optionally contains the other part of the recognition sequence of the restriction enzyme from step aa), ba) or a),

c) a solid matrix,

d) reservoirs for the enzymes required to produce the nucleic acid molecule and/or other reagents and,

e) a control program which can identify individual oligonucleotides from aa), ba) or a) and ab), bb) or b), contact them with the solid matrix from ac), bc) or c) and with the required enzymes and/or other reagents from ad), bd) or d) and determine and carry out the sequence of synthesis steps.